**Amendments to the Claims**

Please amend claims 1-4, 11, 12,18-22, 25, and 26 as indicated in the listing of claims.

The listing of claims will replace all prior versions, and listings of claims in the application.

**Listing of Claims:**

1. (Currently amended) A method for detecting the presence of a mammalian [~~mutant~~] target neoplastic nucleic acid having a mutant nucleotide sequence in a neoplasm and in a tumor margin tissue specimen comprising,

extracting the nucleic acid present in the neoplasm and in the tumor margin tissue specimen, wherein the tissue specimen is external to a primary neoplasm, and wherein the tissue specimen is histologically normal [~~wherein the nucleic acid is selected from APC, DCC, NF1, NF2, RET, VHL, and WT-1~~]; and

detecting the mutant nucleotide sequence in the nucleic acid [[in]] extracted from the neoplasm and in the nucleic acid extracted from the [~~histologically normal~~] tissue specimen, [~~wherein the specimen is external to a primary neoplasm~~] wherein the target neoplastic nucleic acid is selected from APC, DCC, NF1, NF2, RET, VHL, and WT-1, and wherein the mutant nucleotide sequence is present in the primary neoplasm.

2. (Currently amended) The method of claim 1, further comprising, prior to detecting [~~the presence of~~] the mutant [~~target nucleic acid~~] nucleotide sequence, amplifying the nucleic acid [~~present in~~] extracted from the tissue specimen to produce an amplified nucleic acid, wherein said detecting comprises detecting the presence of the mutant [~~target nucleic acid~~] nucleotide sequence in the amplified nucleic acid.

3. (Currently amended) The method of claim 2, wherein said amplifying is by means of oligonucleotides that hybridize to flanking regions of the mutant [~~target nucleic acid~~] nucleotide sequence.

4. (Currently amended) The method of claim 1, wherein the mutant [~~target nucleic acid~~] nucleotide sequence contains a mutation selected from the group consisting of a restriction fragment length polymorphism, a nucleic acid deletion, and a nucleic acid substitution.

Claims 5- 6. (Canceled).

7. (Previously presented) The method of claim 1, wherein the neoplasm is a neoplasm of the head or a neoplasm of the neck.

8. (Previously presented) The method of claim 1, wherein the neoplasm is head and neck cancer.

9. (Previously presented) The method of claim 1, wherein the neoplasm is a benign neoplasm.

10. (Previously presented) The method of claim 1, wherein the neoplasm is a malignant neoplasm.

11. (Currently amended) The method of claim 2, further comprising, prior to detecting [~~the presence of~~] the mutant [~~nucleic acid~~] nucleotide sequence, cloning the amplified nucleic acid, wherein said detecting comprises detecting the presence of the mutant [~~target nucleic acid~~] nucleotide sequence in the amplified nucleic acid.

12. (Currently amended) A method for detecting metastases in a subject having an excised tumor, the method comprising:

a) isolating tissue from a surgical margin adjacent to the excised tumor, wherein the tissue is histologically normal;

b) contacting the tissue with an oligonucleotide that specifically hybridizes to a mammalian target neoplastic nucleic acid [~~sequence~~] having a [~~mutation~~] mutant nucleotide sequence, wherein the target neoplastic nucleic acid is selected from [~~at least~~] APC, DCC, NF1, NF2, RET, VHL, and WT-1, and wherein the mutant nucleotide sequence is present in the primary neoplasm; and

c) detecting the presence of the [~~nucleic acid~~] mutant nucleotide sequence, wherein the presence of the [~~nucleic acid~~] mutant nucleotide sequence is indicative of metastases.

13. (Canceled).

14. (Previously presented) The method according to claim 12 wherein the tissue is normal under a microscope.

Claims 15- 17. (Canceled).

18. (Currently amended) A method for detecting a mammalian target neoplastic nucleic acid having a mutant nucleotide sequence in a tissue specimen which is external to a primary neoplasm, comprising isolating a tissue specimen wherein the tissue specimen is histologically normal, extracting nucleic acid present in the tissue specimen to obtain extracted nucleic acid, [~~isolating a tissue specimen wherein the tissue specimen is histologically normal,~~] and detecting the presence of the [~~target mutant neoplastic nucleic acid~~] mutant nucleotide sequence in the extracted nucleic acid and in the tissue specimen, wherein the target [~~mutant~~] neoplastic nucleic acid is selected from APC, DCC, NF1, NF2, RET, VHL, and WT-1, and wherein the mutant nucleotide sequence is present in the primary neoplasm.

19. (Currently amended) A method for detecting a mammalian target neoplastic nucleic acid having a mutant nucleotide sequence in a tumor margin tissue specimen which is external to a primary neoplasm, comprising isolating a tissue specimen wherein the tissue specimen appears histologically normal, extracting nucleic acid present in the tissue specimen to obtain extracted nucleic acid, [~~isolating a tissue specimen wherein the tissue specimen appears histologically normal,~~] and detecting the presence of the [~~target neoplastic nucleic acid~~] mutant nucleotide sequence in the extracted nucleic acid, wherein the target [~~mutant~~] neoplastic nucleic acid is selected from APC, DCC, NF1, NF2, RET, VHL, and WT-1, and wherein the mutant nucleotide sequence is present in the primary neoplasm.

20. (Currently amended) A method for detecting the presence of a mammalian [~~mutant~~] target neoplastic nucleic acid having a mutant nucleotide sequence in a neoplasm and in a lymph node tissue specimen, comprising:

isolating a lymph node tissue specimen wherein the tissue specimen is external to a primary neoplasm, and wherein the tissue specimen appears histologically normal

extracting [~~mutant~~] nucleic acid present in the neoplasm and in the tissue specimen and, wherein the [~~mutant~~] target neoplastic nucleic acid is selected from APC, DCC, NF1, NF2, RET, VHL, and WT-1, and wherein the mutant nucleotide sequence is present in the primary neoplasm;

[~~isolating a tissue specimen wherein the tissue specimen is external to a primary neoplasm, and wherein the tissue specimen appears histologically normal;~~] and

detecting the mutant [~~target nucleic acid~~] nucleotide sequence in the extracted nucleic acid from the neoplasm and in the extracted nucleic acid from the tissue specimen.

21. (Currently amended) The method of claim 20, further comprising, prior to detecting [~~the presence of~~] the mutant [~~target nucleic acid~~] nucleotide sequence, amplifying the extracted nucleic acid [~~present in the~~] from the tissue specimen to produce an amplified nucleic acid, wherein said detecting comprises detecting the presence of the mutant [~~target nucleic acid~~] nucleotide sequence in the amplified nucleic acid.

22. (Currently amended) The method of claim 20, wherein the mutant [~~target nucleic acid~~] nucleotide sequence contains a mutation selected from the group consisting of a restriction fragment length polymorphism, a nucleic acid deletion, and a nucleic acid substitution.

23. (Canceled).

24. (Previously presented) The method of claim 20, wherein the neoplasm is a neoplasm of the head or a neoplasm of the neck.

25. (Currently amended) A method for detecting metastases in a subject having an excised tumor, the method comprising:

a) isolating tissue from a lymph node, which is external to a primary neoplasm and appears histologically normal;

b) [~~applying to said~~] contacting the tissue with an oligonucleotide that specifically hybridizes to a mammalian target neoplastic nucleic acid having a mutant nucleotide sequence, wherein the target neoplastic nucleic acid is selected from APC, DCC, NF1, NF2, RET, VHL, and WT-1, and wherein the mutant nucleotide sequence is present in the primary neoplasm; and

c) detecting the presence of [~~said neoplastic nucleic acid~~] the mutant nucleotide sequence, wherein the presence of [~~said neoplastic nucleic acid~~] the mutant nucleotide sequence indicates metastases.

26. (Currently amended) The method of claim 25, wherein no more than an average of about one out of every ten thousand cells of said tissue have a [~~neoplastic nucleic acid~~] mutant nucleotide sequence.

Claims 27-31. (Canceled).